Whole-genome shotgun sequencing of three listeria monocytogenes strains isolated from a ready-to-eat salad-producing facility in Switzerland

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Abstract: Ready-to-eat (RTE) raw foods harbor the risk of transmitting Listeria monocytogenes from the environment to the consumer. We isolated three strains from a facility producing RTE salad. These strains were used to perform challenge tests on different RTE salad products. Here, we present the shotgun genome sequences of all three of these strains.

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Whole genome shotgun sequencing of three *L. monocytogenes* strains isolated from a ready-to-eat salad producing facility in Switzerland.

Matthias Ziegler[a], Hyein Jang[b], Gopal Gopinath[b], Jule Anna Horlbog[a] Roger Stephan[a], Claudia Guldimann [a#]

[a] Institute for Food Safety and Hygiene, Vetsuisse Faculty, University of Zürich, Switzerland

[b] Center of Food Safety and Applied Nutrition, U. S. Food and Drug Administration, Laurel, MD 20708 USA.

Running title: "Three strains of *L. monocytogenes* isolated from RTE salads"

address correspondence to: Claudia Guldimann, Institute for Food Safety and Hygiene, Vetsuisse Faculty, University of Zürich, Winterthurerstr. 272, 8057 Zürich, Switzerland; claudia.guldimann@uzh.ch

Abstract

Ready-to-eat (RTE) raw foods harbour the risk of transmitting *Listeria monocytogenes* from the environment to the consumer. We isolated three strains from a RTE salad producing facility. These strains were used to perform challenge tests on different RTE salad products. Here we present the shotgun genome sequences of all three strains.

Genome announcement

Genomic DNA from *L. monocytogenes* N16-0716, N16-0855 and N16-1125 was extracted from a BHI culture using a DNA blood and tissue kit (Qiagen) and subjected to whole-genome sequencing using the MiSeq platform (Illumina, San Diego, CA, USA) and a Nextera XT library kit utilizing either 500 or 600 cycles of paired-end reads (Illumina). The paired end libraries were generated and sequenced in conjunction with the Nextera XT DNA sample preparation guide on the Illumina Miseq instrument (Illumina; San Diego, CA) (1). The reads were de novo assembled with Spades, version 3.11 (2) into genomes of 2968449 bp, 37.9% CG (N16-0716), 3138349bp, 38.8% CG (N16-0855), and 3124080bp, 38.6% GC (N16-1125). The genomes were annotated using the RAST (3) annotation server, and 2931 (N16-0716), 3072 (N16-0855), and 3078 (N16-1125) coding sequences were identified, respectively.

MLST analysis on http://bigsdb.pasteur.fr/listeria/ confirmed our earlier, PCR-based analysis that N16-0716 was ST517 CC517, N16-0855 was ST6 CC6, and N16-1125 was ST91 CC14. An analysis of known virulence genes in comparison to the laboratory strain 10403S revealed that all genes associated with the LIPI-1 island were present in all three strains. In all three strains, *plcB* was present in full length with several amino acid (aa) substitutions between the strains. The alternative start codon GTG was used in *plcB* all three strains (as well as in 10403S). All other genes on LIPI-1 were present in full length and none of the known *prfA** mutations were detected. Two different alleles of *hly* were present between the strains, separated by four aa substitutions. In *plcA*, *mpl* and *actA*, several aa substitutions were detected between the strains. *ilsA* coding for listeriolysin S on LIPI-3 was only found in N16-0855. InlA was present in full length in all sequences with several aa substitutions between the strains.

Screening of the genomes against the ARGANNOT (4) and megares (5) databases of antimicrobial resistance (AMR) genes using the method described by Carroll, et al. (6) and implemented in BTyper v. 2.2.0 (7) revealed the multidrug efflux pumps *norB, msrA* and *mepA* in all three strains.

Phaster (8) identified two intact phages in N16-0716, two intact and one incomplete phage in N16-0855 and four intact phages on N16-1125.

Accession numbers: this Whole Genome Shotgun project has been deposited in GenBank under the accession no. QELV00000000 (N16-0716), QELU00000000 (N16-0855) and QELT00000000 (N16-1125).

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